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 201 CAGAGGGGGCACCTGGTCGGACTCGGTTGGGCTCGGGCGGCCCCGCCTCCCCCCGCCCGCCAGGCGGGCCCTTCTCGACGGCGCGGGGCGGGCCCTGCGG

 301 GCGCGGGGCTGAAGGCGGAACCACGACGGGCAGAGAGCACGGAGCCGGGAAGCCCCTGGGCGCCCGTCGGAGGGCTATGGAGCAGCGGCCGCGGGGCTGC
   1                                                                                   M  E  Q  R  P  R  G  C

 401 GCGGCGGTGGCGGCGGCGCTCCTCCTGGTGCTGCTGGGGGCCCGGGCCCAGGCCGGCACTCGTAGCCCCAGGTGTGACTGTGCCGGTGACTTCCACAAGA
   9  A  A  V  A  A  A  A  L  L  L  V  L  L  G  A  R  A  Q  G  G  T  R  S  P  R  C  D  C  A  G  D  F  H  K  K

 501 AGATTCGTCTGTTTTGTTGCAGAGGCTGCCCAGCGGGGCACTACCTGAAGGCCCCTTGCACGGAGCCCTGCGGCAACTCCACCTGCCTTGTGTGTCCCCA
  43     I  C  L  F  C  C  R  G  C  P  A  G  H  Y  L  K  A  P  C  T  E  P  C  G  N  S  T  C  L  V  C  P  Q

 601 AGACACCTTCTTGGCCTGGGAGAACCACCATAATTCTGAATGTGCCCGCTGCCAGGCCTGTGATGAGCAGGCCTCCCAGGTGGCGCTGGAGAACTGTTCA
  76  D  T  F  L  A  W  E  N  H  H  N  S  E  C  A  P  C  Q  A  C  D  E  Q  A  S  Q  V  A  L  E  N  C  S

 701 GCACTGGCCGACACCCGCTGTGGCTGTAAGCCAGGCTGGTTTGTGGAGTGCCAGGTCAGCCAATGTGTCAGCAGTTCACCCTTCTACTGCCAACCATGCC
 109  A  V  A  D  T  R  C  G  C  K  P  G  W  F  V  E  C  Q  V  S  Q  C  V  S  S  S  P  F  Y  C  Q  P  C  L

 801 TAGACTGCGGGGCCCTGCACCGCCACACACGGCTACTCTGTTCCCGCAGAGATACTGACTGTGGGACCTGCCTGCCTGGCTTCTATGAACATGGCGATGG
 143    D  C  G  A  L  H  R  H  T  R  L  L  C  S  R  R  D  T  D  C  G  T  C  L  P  G  F  Y  E  H  G  D  G

 901 CTGCGTGTCCTGCCCCACGTAATTCCTAGCTGTCGTGGGATGGAGGGAAGGGCCGCTGGGAGCAGAGCAGGGGCCTGGGGTGGGGCAGGTGCTGCTGGTT
 176  C  V  S  C  P  T

1001 CAGGAATAGGAAGAGGGGATAGGGAGGAGGGAGCCTTGGCCCTGTGATGGGTGGGCCCCACTTCAGGCAAACTTAGATGGCAAAAGAGCAATCTGGATCC

1101 GCCTTAGCCAGATACATAAGGGTATTTGCCTTCACTTTCAGCCAGCATTCCCCCCAGCGATCCTAGCCAGATATTACAGATGATTTGTCACTTACACAGA

1201 GAGTCACATTGATATAGCTTTAAAACTTGGGCTGAAGGAGGTTGAGGCTGCAGTGAGCTATGATCGTGCCACTGCACTTCAGCCTGGGCAACAGAGCGAG

1301 ACCTATTAAATAAATAAATAAATATTAAATCTATTAAATATTAAATATTAAATCTATTAAATAAATAAATACAAAGGGCTGAGAGTCAGGACTGTGCTGC

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FIG. 1

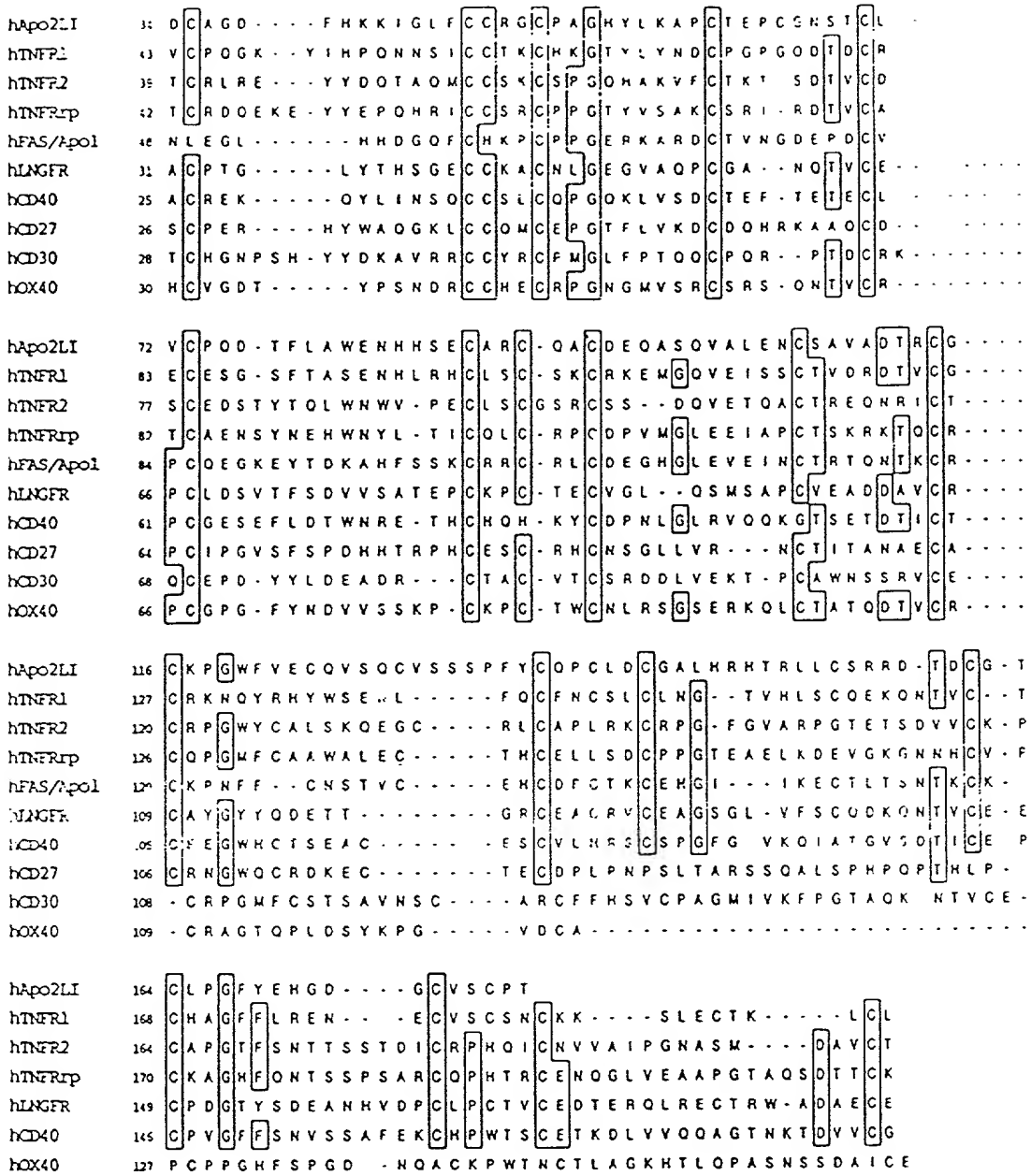
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Fig. 2

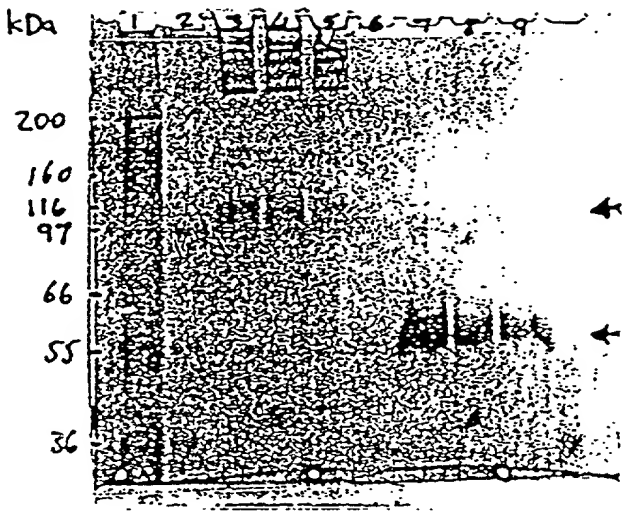

Fig. 3

DOCKET NO. 26660

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   1                                  M  E  Q  R  P  R  G  C  A  A  V
 121 GGCGGCGGCG CTCCTCCTGG TGCTGCTGGG GGCCCGGGCC CAGGGCGGCA CTCGTAGCCC
  12  A  A  A  L  L  L  V  L  L  G  A  R  A  Q  G  G  T  R  S  P
 181 CAGGTGTGAC TGTGCCGGTG ACTTCCACAA GAAGATTGGT CTGTTTTGTT GCAGAGGCTG
  32  R  C  D  C  A  G  D  F  H  K  K  I  G  L  F  C  C  R  G  C
 241 CCCAGCGGGG CACTACCTGA AGGCCCCTTG CACGGAGCCC TGCGGCAACT CCACCTGCCT
  52  P  A  G  H  Y  L  K  A  P  C  T  E  P  C  G  N  S  T  C  L
                                                   *
 301 TGTGTGTCCC CAAGACACCT TCTTGGCCTG GGAGAACCAC CATAATTCTG AATGTGCCCG
  72  V  C  P  Q  D  T  F  L  A  W  E  N  H  H  N  S  E  C  A  R
 361 CTGCCAGGCC TGTGATGAGC AGGCCTCCCA GGTGGCGCTG GAGAACTGTT CAGCAGTGGC
  92  C  Q  A  C  D  E  Q  A  S  Q  V  A  L  E  N  C  S  A  V  A
                                                   *
 421 CGACACCCGC TGTGGCTGTA AGCCAGGCTG GTTTGTGGAG TGCCAGGTCA GCCAATGTGT
 112  D  T  R  C  G  C  K  P  G  W  F  V  E  C  Q  V  S  Q  C  V
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 132  S  S  S  P  F  Y  C  Q  P  C  L  D  C  G  A  L  H  R  H  T
 541 ACGGCTACTC TGTTCCCGCA GAGATACTGA CTGTGGGACC TGCCTGCCTG GCTTCTATGA
 152  R  L  L  C  S  R  R  D  T  D  C  G  T  C  L  P  G  F  Y  E
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 172  H  G  D  G  C  V  S  C  P  T  S  T  L  G  S  C  P  E  R  C
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 721 GGTCCCCCTC CTGCTTGGGG CCACCCTGAC CTACACATAC CGCCACTGCT GGCCTCACAA
 212  V  P  L  L  L  G  A  T  L  T  Y  T  Y  R  H  C  W  P  H  K
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 232  P  L  V  T  A  D  E  A  G  M  E  A  L  T  P  P  P  A  T  H
 841 TCTGTCACCC TTGGACAGCG CCCACACCCT TCTAGCACCT CCTGACAGCA GTGAGAAGAT
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 312  A  A  P  T  L  S  P  E  S  P  A  G  S  P  A  M  M  L  Q  P
1081 GGGCCCGCAG CTCTACGACG TGATGGACGC GGTCCCAGCG CGGCGCTGGA AGGAGTTCGT
 332  G  P  Q  L  Y  D  V  M  D  A  V  P  A  R  R  W  K  E  F  V
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1621 AAAAAAAAAA AAAA
```

Fig. 4

```
Apo3       1 MEQRPRGCAAVAAALLLVLLGARAQGGTRSPR------------
TNFR1      1 MGLSTVPDLLLPL-VLLELLVGIYPSGVIGLVPHLGDREKRDSV
Fas/Apo1   1 MLGIWTLLPLVLTSVARLSSKSVNAQVTDINSKGLELRKTVTTV

Apo3      33 CDCAGDFHKKIGLFCCRGCPAGHYLKAPCTEPCGNSTCLV
TNFR1     44 CPQGKYIHPQNNSICCTKCHKGTYLYNDCPGPGQDTDCRE
Fas/Apo1  45 ETQNLEGLHHDGQFCHKPCPPGERKARDCTVNGDEPDCVP

Apo3      73 CPQDTFLAWENHHNSECARCQACDEQASQVALENCSAVADTRCG
TNFR1     85 CESGSFTASENHLRH-CLSCSKCRKEMGQVEISSCTVDRDTVCG
Fas/Apo1  85 CQEGKEYTDKAHFSSKCRRCRLCDEGHGLEVEINCTRTQNTKCR

Apo3     117 CKPGWFVECQVSQCVSSSPFYCQPCLDCGALHRHTRLLCSRRD-TDCGT
TNFR1    127 CRKNQYRHYWSENLFQ-----CFNCSLCLNGTVHLS--CQEKQNTVCT-
Fas/Apo1 129 CKPNFF--CNSTVCEH-----CDPCTKCEHGIIKE---CTLTSNTKCKE

Apo3     165 CLPGFYEHGDGCVSCPTSTLGSCP--ERCAAVCGW
TNFR1    168 CHAGFFLRENECVSCS-----NCKKSLECTKLCLP

Apo3     338 VMDAVPARRWKEFVRTLGLREAEIEAVEVEIGR--FRDQQYE
TNFR1    333 VVENVPPLRWKEFVRRLGLSDHEIDRLELQNGR-CLREAQYS
Fas/Apo1 220 IAGVMTLSQVKGFVRKNGVNEAKIDEIKNDNVQDTAEQKV-Q
FADD     104 ICDNVGK-DWRRLARQLKVSDTKIDSIEDRYPRN-LTERVRE
TRADD    211 NRPLSLK-DQQTFARSVGLKWRKVGR-SLQRGCRALRDPALD
RIP      291 IRENLGK-HWKNCARKLGFTQSAIDEIDHDYERDGLKEKVYQ
Reaper     1                MAVAFYIPDQATLLREAEQKEQQILR-LRESQWR

Apo3     378 MLKRWRQQQP---AGLGAVYAALERMGL-DGCVEDLRS
TNFR1    374 MLATWRRRTPRREATLELLGRVLRDMDL-LGCLEDIEE
Fas/Apo1 261 LLRNWHQLHG-KKEAYDTLIKDLKKANLCTLA-EKIQT
FADD     144 SLRIWKNTE-KENATVAHLVGALRSC---QMNLVADLV
TRADD    251 SLAYEYEREGLYEQAFQLLRRFV-QAEGRRATLQRLVE
RIP      332 MLQKWVMREGIKGATVGKLAQALHQC--SRIDLLSSLT
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Fig. 5

Fig. 6

TOGETHER-WE2E6660

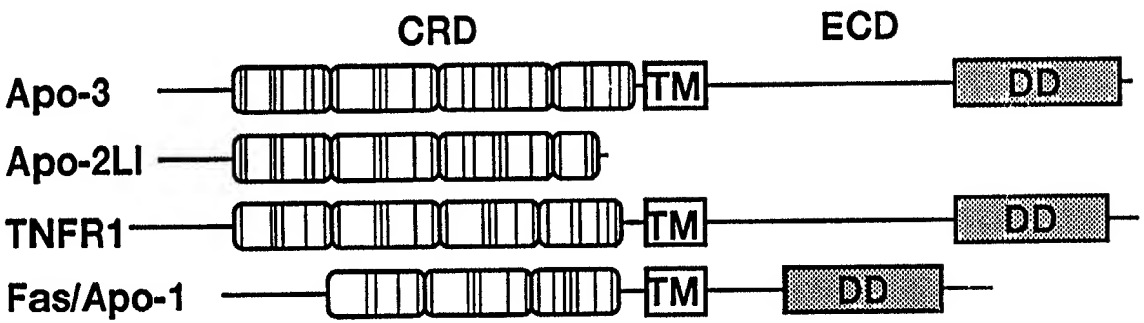


Fig. 7

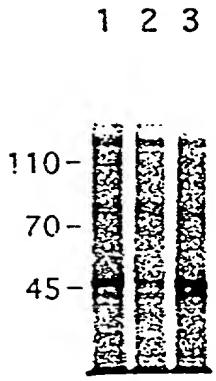
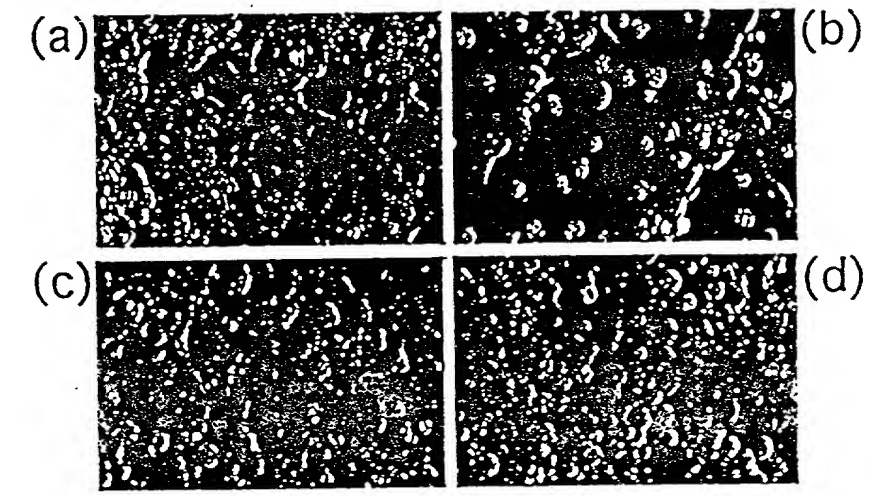


Fig. 8

Fig. 9



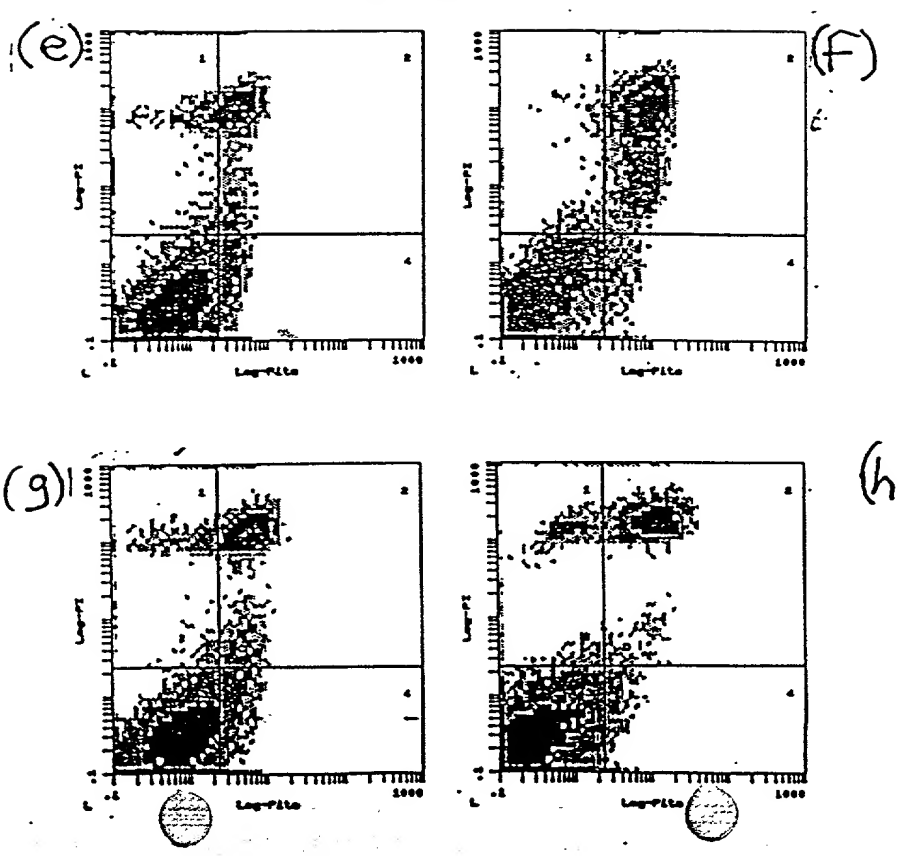
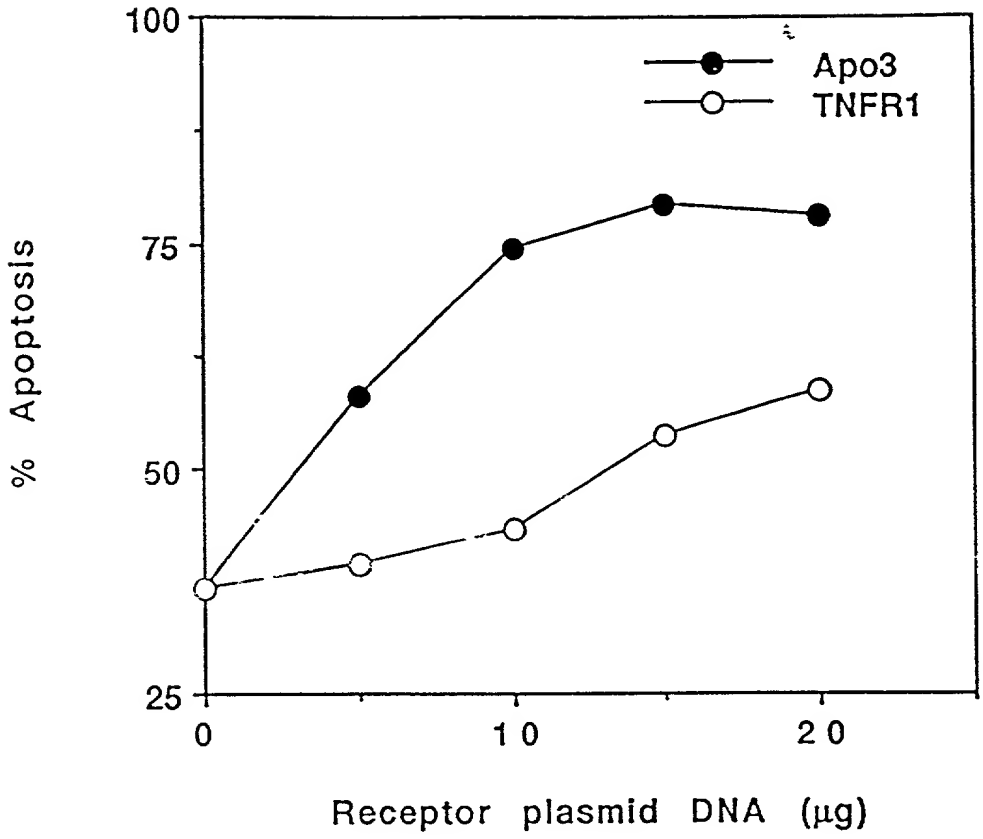


Fig. 9i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75
50
25
% Apoptosis
Apo3
TNFR1
0
10
20
Receptor plasmid DNA (µg)

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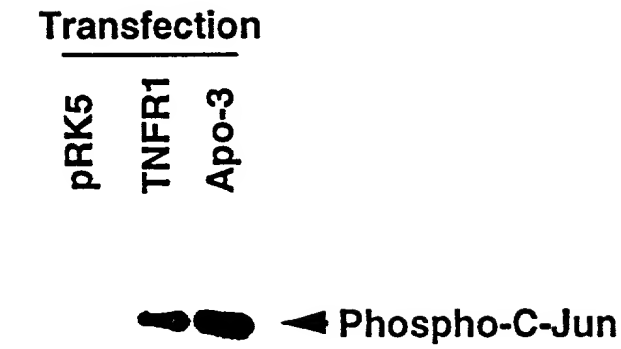
Fig. 10



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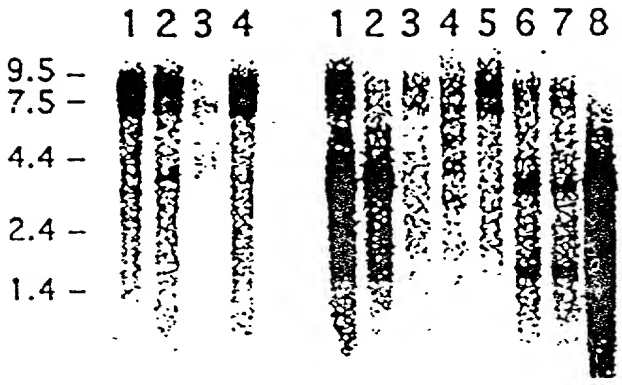

Fig. 12